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5 - 6 - 7, Minamino

Hachioji-shi

192-0916, TOKYO, XX (JP).

(71) YAMAUCHI, YOSHIO,
403 - 3 - 22 - 13, Higashi-toyoda
Hino-shi
191-0052, TOKYO, XX (JP).
SHINKAWA, TAKASHI,
7 - 27 - 23, Kamaitsuruma-honchou
Sagamihara-shi
228-0801, KANAGAWA, XX (JP).
ISOBE, TOSHIAKI,

(72)

YAMAUCHI, YOSHIO (JP).
SHINKAWA, TAKASHI (JP).
ISOBE, TOSHIAKI (JP).

(74)

GOWLING LAFLEUR HENDERSON LLP

(54) PROCEDE D'ANALYSE DE PROTEINES

(54) PROTEIN ANALYSIS METHOD

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It is intended to provide a protein analysis method whereby proteins can be identified and the quantification data can be obtained by a convenient procedure. Namely, a protein analysis method characterized by comprising: the step of cleaving two protein-containing samples individually with restriction enzymes at specific amino acid sites to give peptide chain-containing samples; the step of modifying peptide chains contained in the peptide chain-containing samples with labeling compounds having different masses due to isotopes so as to impart different masses to the peptide chains; the step of mixing the isotope-labeled peptide chain-containing samples and fractionally quantifying the sample mixture for individual peptide chains so as to determine a content ratio; the step of selecting peptide chains to be subjected to amino acid sequence identification from the peptide chains and identifying the amino acid sequences of the peptide chains; the step of specifying proteins corresponding to the peptide chains; and the step of determining the content ratio of the thus specified proteins based on the fractional quantification data of the peptide chains.

